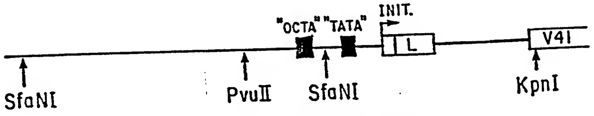


MOPC-41 κ CHAIN GENE

FIG.1A

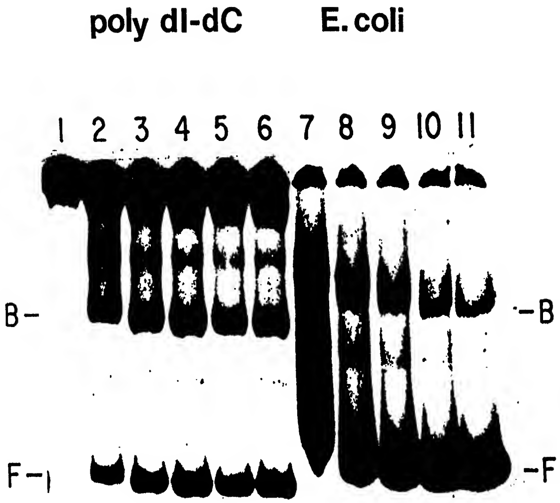


FIG.1B

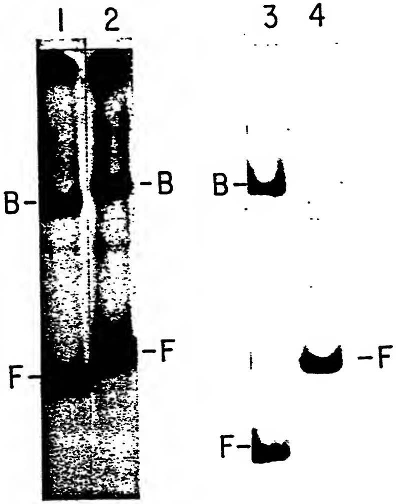


FIG. 1C

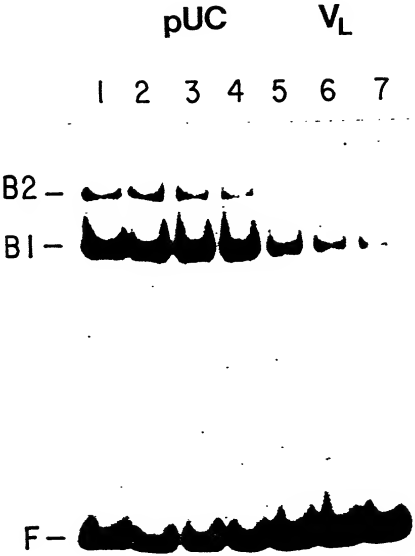
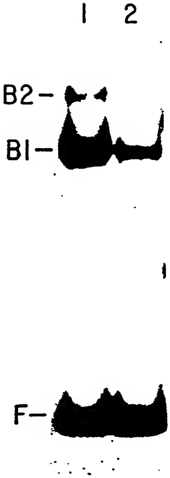


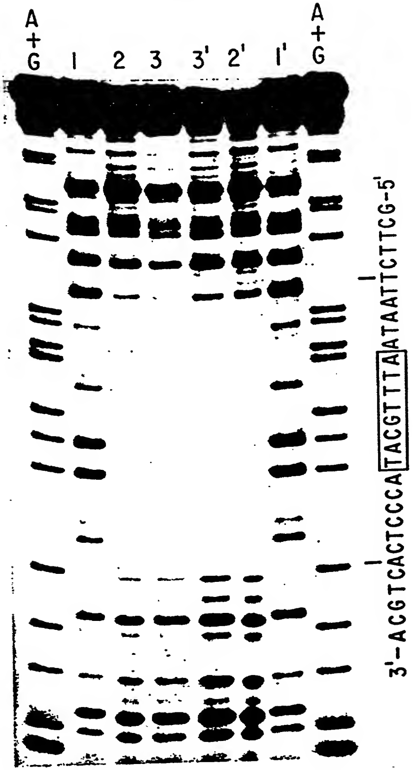
FIG.2A

FIG.2B



Hela

FIG.3



V_L coding strand (-66)	TC$\overset{*}{T}$TAATA	ATTTGCAT	ACCCTC$\overset{*}{A}$C
V_H non-coding strand (-50)	CGCACATG	ATTTGCAT	ACTCATGA
J_H-$C\mu$ coding strand (166)	CCTGGGTA	ATTTGCAT	TTCTAAAA

FIG.4A

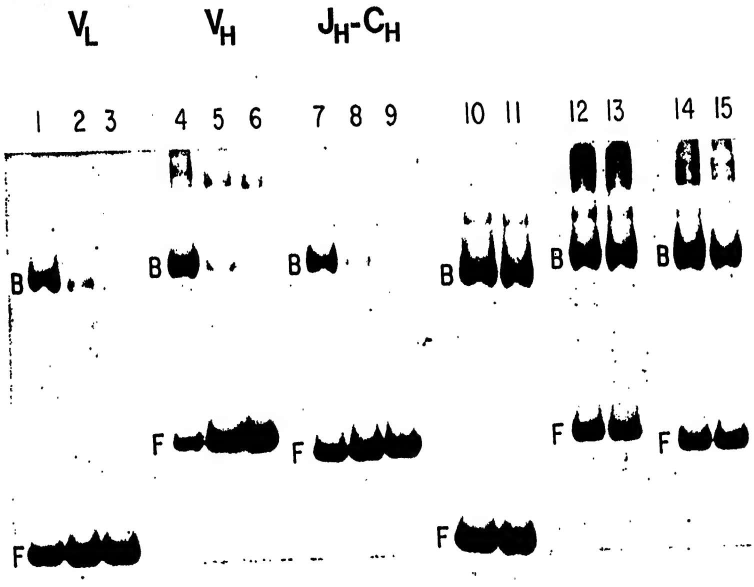


FIG.4B

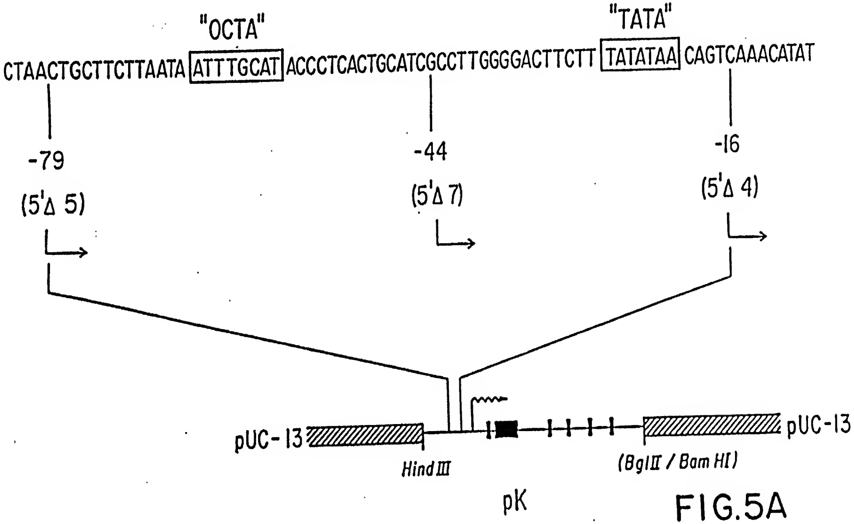
"OCTA"
"TATA"
CTAACTGCTTCTTAATA ATTTGCAT ACCCTCACTGCATCGCCTTGGGGACTTCTT TATATAA CAGTCAAACATAT
-79
(5'Δ 5)
-44
(5'Δ 7)
-16
(5'Δ 4)
pUC-13
HindIII
pK
(BglII / BamHI)
pUC-13

FIG.5A

FIG.5B

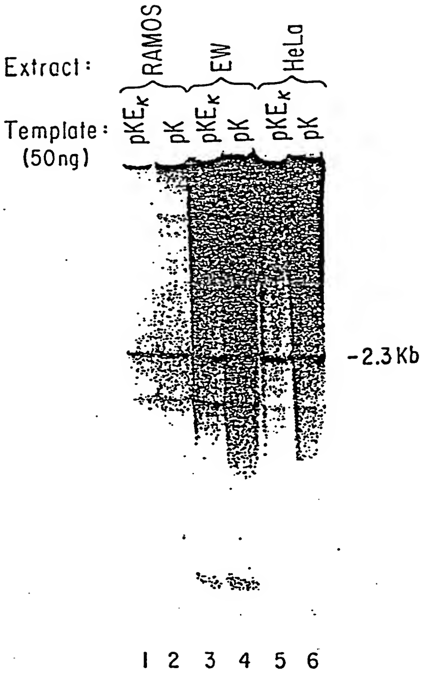

Extract:
RAMOS
EW
HeLa
Template:
(50ng)
pKEκ
pK
pKEκ
pK
pKEκ
pK
-2.3Kb
1 2 3 4 5 6

FIG.6

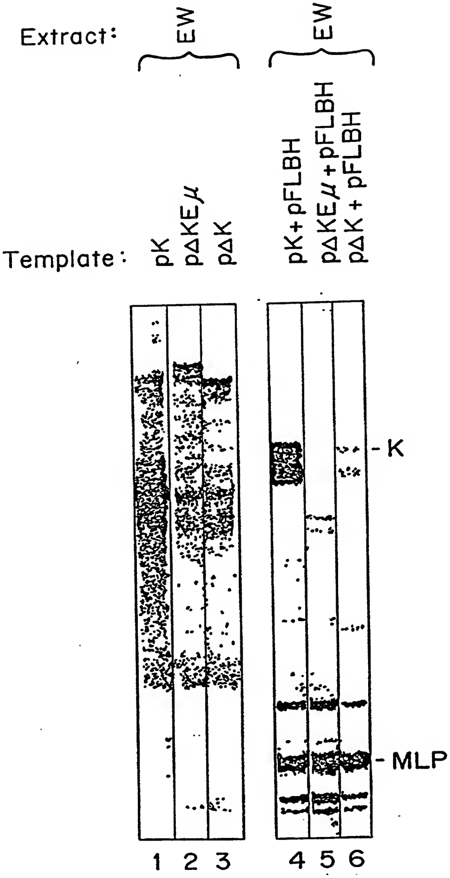

Extract:
EW
EW
Template:
pK
pΔKEμ
pΔK
pK+pFLBH
pΔKEμ+pFLBH
pΔK+pFLBH
-K
-MLP
1
2
3
4
5
6

FIG.7

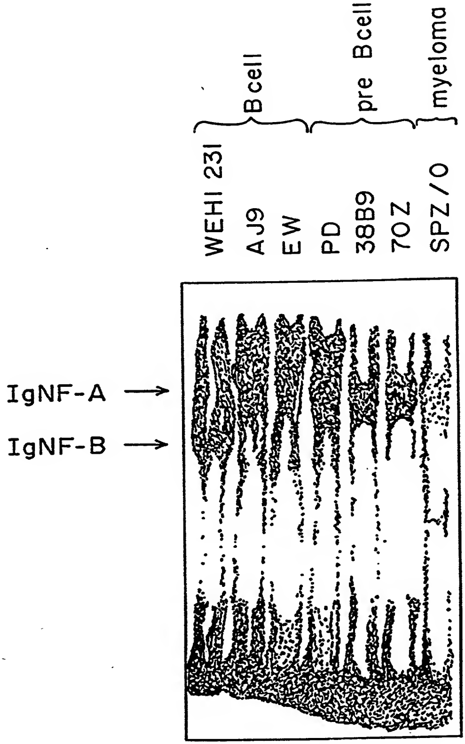
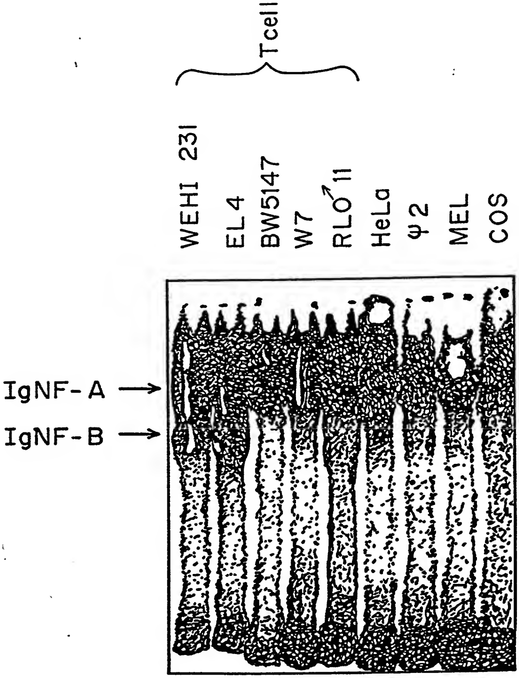

WEHI 231
AJ9
EW
PD
38B9
70Z
SPZ/0
B cell
pre Bcell
myeloma
IgNF-A
IgNF-B

FIG.8



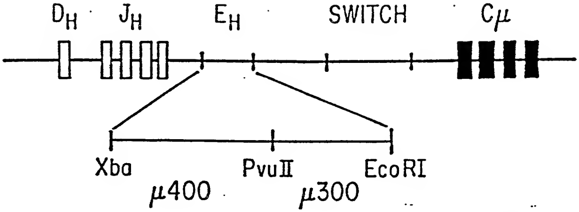

D_H
J_H
E_H
SWITCH
Cμ
Xba
PvuII
EcoRI
μ400
μ300

FIG.9A

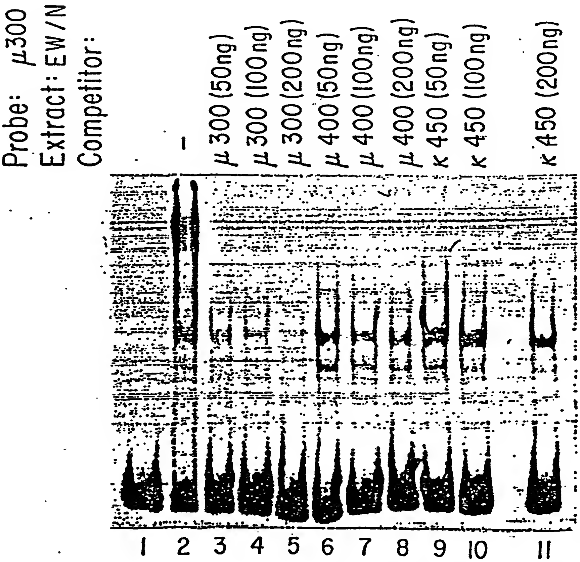

Probe: μ300
Extract: EW/N
Competitor:
-
μ 300 (50ng)
μ 300 (100ng)
μ 300 (200ng)
μ 400 (50ng)
μ 400 (100ng)
μ 400 (200ng)
κ 450 (50ng)
κ 450 (100ng)
κ 450 (200ng)
1
2
3
4
5
6
7
8
9
10
11

FIG.9B

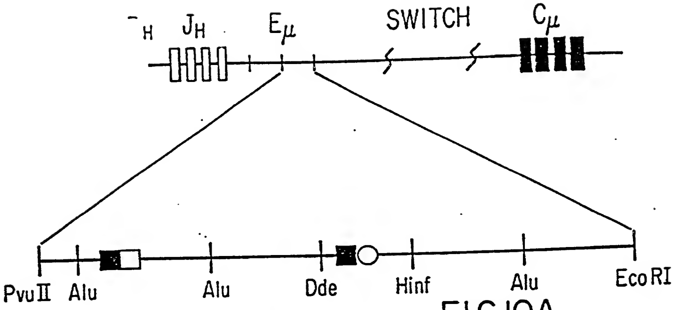


FIG.10A

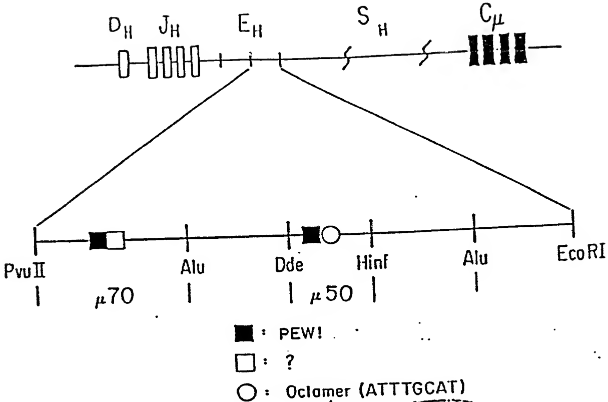
■ : E

☐ : ?

○ : Octamer (ATTTGCAT)

FIG.10B

FIG.10C



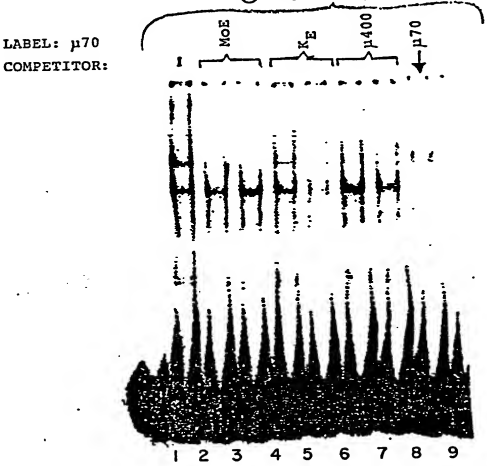


FIG.10D

FIG.10E

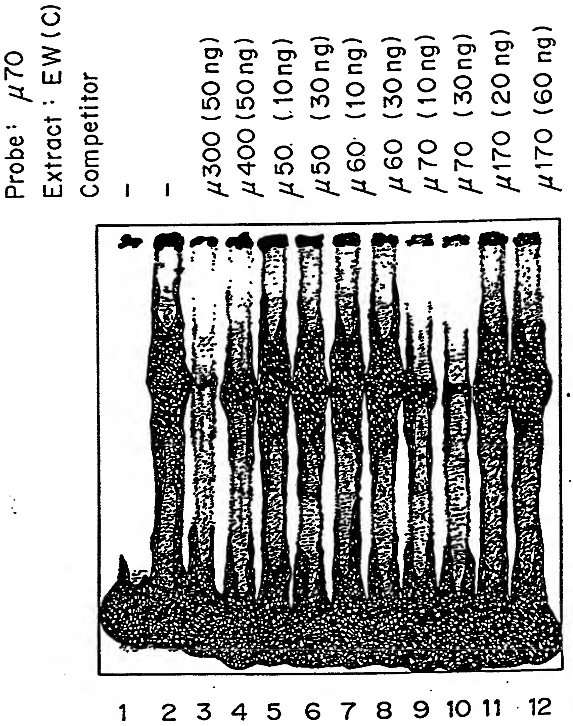

Probe: μ70
Extract : EW(C)
Competitor
-
-
μ300 (50 ng)
μ400 (50 ng)
μ50 (10 ng)
μ50 (30 ng)
μ60 (10 ng)
μ60 (30 ng)
μ70 (10 ng)
μ70 (30 ng)
μ170 (20 ng)
μ170 (60 ng)
1
2
3
4
5
6
7
8
9
10
11
12

FIG.11A

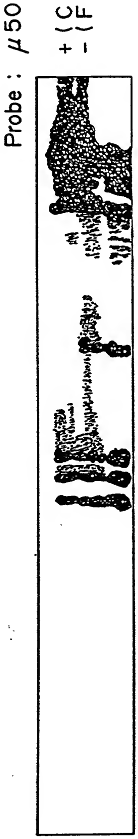
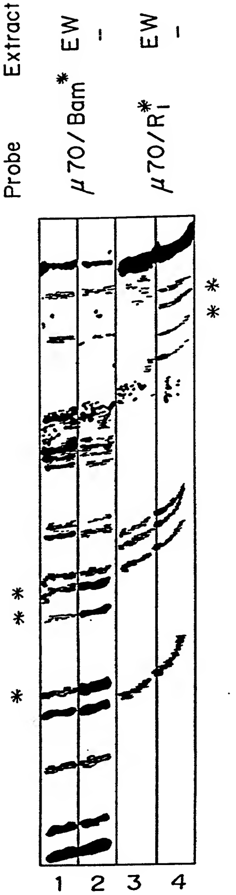


FIG.11B



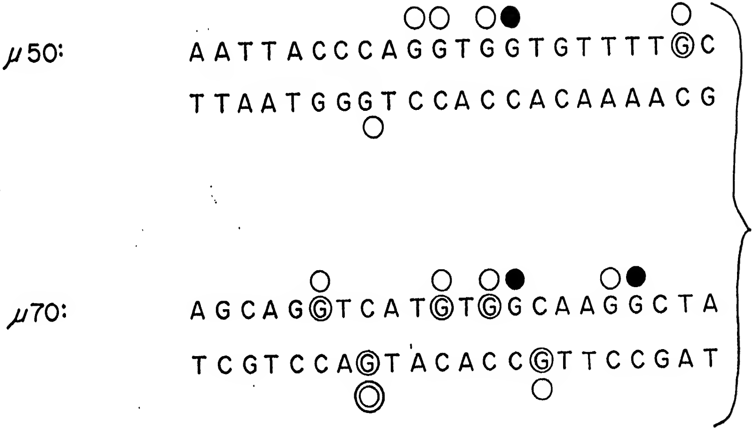
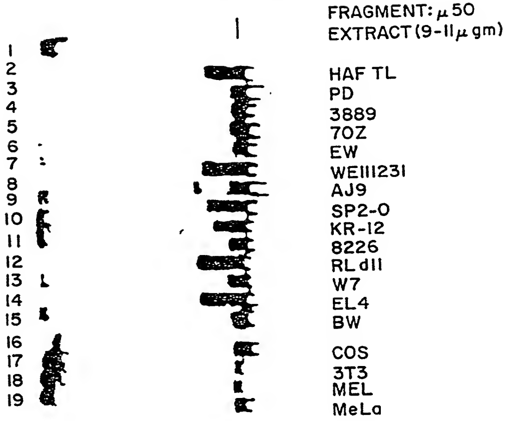

µ50:
AATTACCCAGGTGGTGTTTTGC
TTAATGGGTCCACCACAAAACG
µ70:
AGCAGGTCATGTGGCAAGGCTA
TCGTCCAGTACACCGTTCCGAT

FIG.11C

FIG.12A



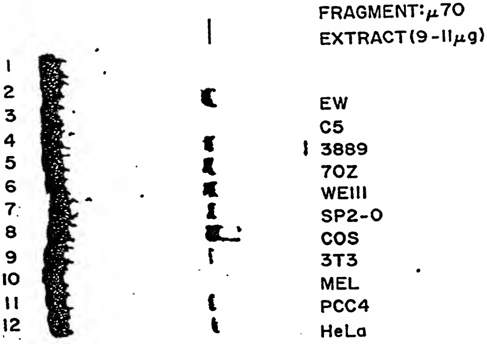


FIG.12B

FIG.13A

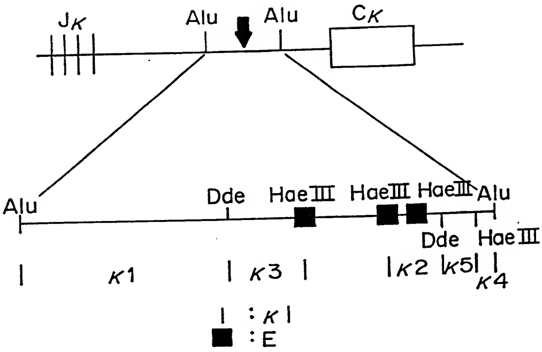


FIG.13B

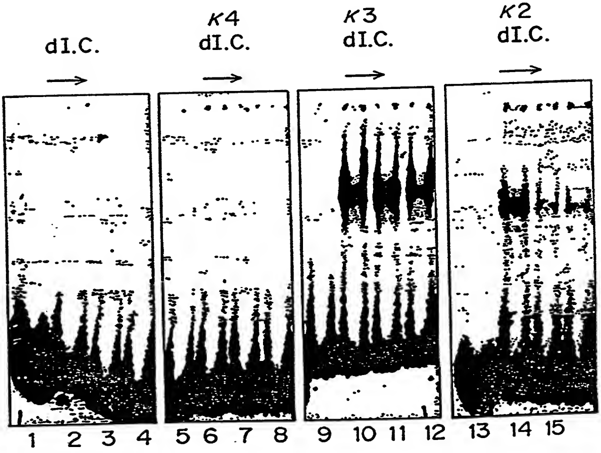
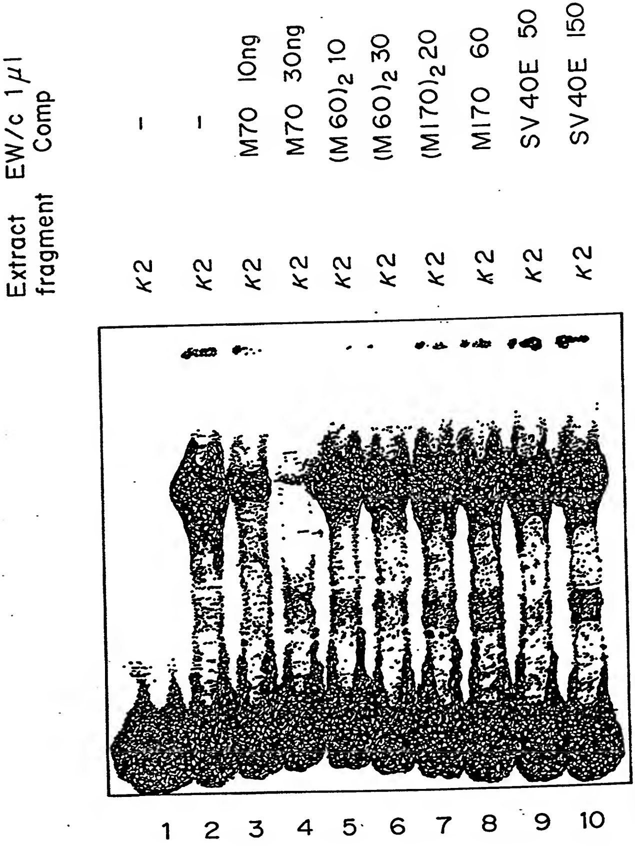


FIG.13C



Extract fragment
EW/c 1μl Comp
κ2 —
κ2 —
κ2 M70 10ng
κ2 M70 30ng
κ2 (M60)2 10
κ2 (M60)2 30
κ2 (M170)2 20
κ2 M170 60
κ2 SV40E 50
κ2 SV40E 150
1
2
3
4
5
6
7
8
9
10

FIG.13D

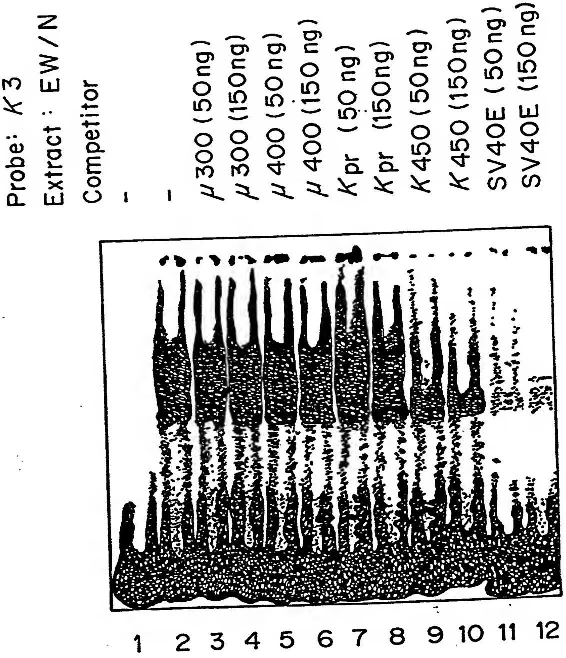

Probe: κ3
Extract : EW/N
Competitor
-
-
μ300 (50ng)
μ300 (150ng)
μ400 (50ng)
μ400 (150 ng)
κpr (50 ng)
κpr (150ng)
κ450 (50ng)
κ450 (150ng)
SV40E (50ng)
SV40E (150ng)
1
2
3
4
5
6
7
8
9
10
11
12

FIG.14

FIG.15A

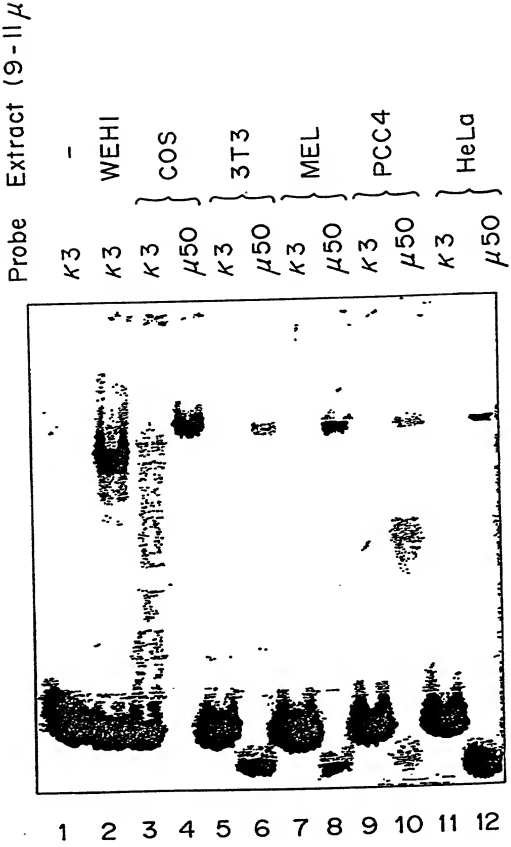

Probe
Extract (9-11μ
κ3
—
κ3
WEHI
κ3
μ50
COS
κ3
μ50
3T3
κ3
μ50
MEL
κ3
μ50
PCC4
κ3
μ50
HeLa
1
2
3
4
5
6
7
8
9
10
11
12

FIG.15B

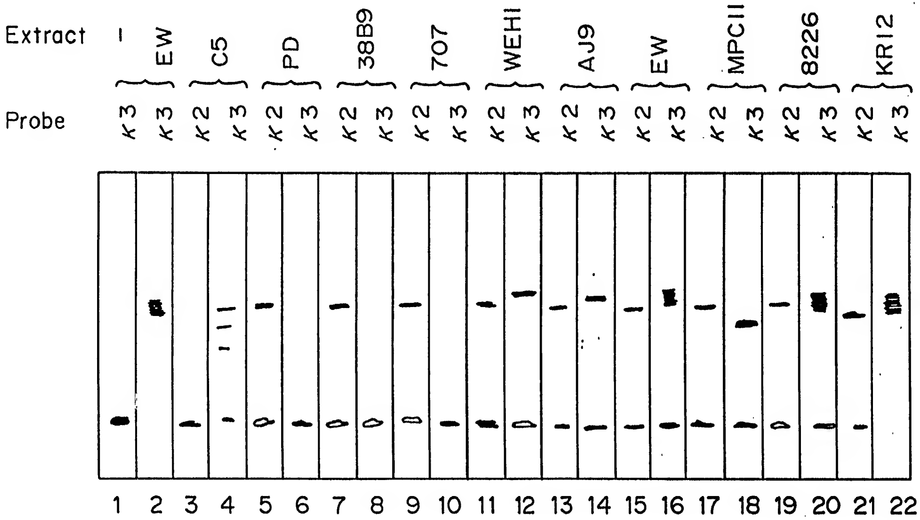

Extract
–
EW
C5
PD
38B9
707
WEHI
AJ9
EW
MPC11
8226
KR12
Probe
κ3
κ3
κ2
κ3
κ2
κ3
κ2
κ3
κ2
κ3
κ2
κ3
κ2
κ3
κ2
κ3
κ2
κ3
κ2
κ3
κ2
κ3
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22

FIG.16

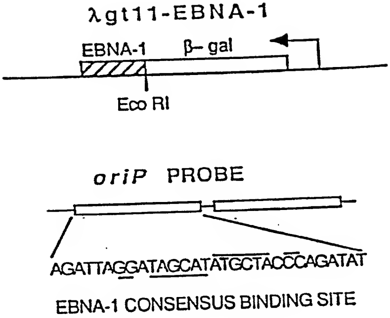

λgt11-EBNA-1
EBNA-1
β- gal
Eco RI
oriP PROBE
AGATTAGGATAGCATATGCTACCCAGATAT
EBNA-1 CONSENSUS BINDING SITE

FIG.17

A.

MHC	$\overline{\text{TGGGGA}}\text{T}\underline{\text{TCCCCA}}$
mhc1	TGcGGATTCCCaA
κEN	aGGGGAcTttCCg
κen	$\text{aaatt}\underset{\text{a}}{\text{A}}\text{cTttCCg}$
SVEN	TGGGGAcTttCCA
HIV	TGGGGAcTttCCA
	aaGGGAcTttCCg

```
    CTGGGGCCCCCAGAGAGGGTGGGGAGATGACACAGTTGTTCCCCCAGCCCTGGCGGGGCG
  1 ---------+---------+---------+---------+---------+---------+

    GGCAGCATGGTTCACTCCAGCATGGGGGCTCCAGAAATAAGAATGTCTAAGCCCCTGGAG
 61 ---------+---------+---------+---------+---------+---------+
          M  V  H  S  S  M  G  A  P  E  I  R  M  S  K  P  L  E

    GCCGAGAAGCAAGGTCTGGACTCCCCATCAGAGCACACAGACACCGAAAGAAATGGACCA
121 ---------+---------+---------+---------+---------+---------+
    A  E  K  Q  G  L  D  S  P  S  E  M  T  D  T  E  R  N  G  P

    GACACTAATCATCAGAACCCCCAAAATAAGACCTCCCCATTCTCCGTGTCCCCAACTGGC
181 ---------+---------+---------+---------+---------+---------+
    D  T  N  H  O  N  P  Q  N  R  T  S  P  F  S  V  S  P  T  G

    CCCAGTACAAAGATCAAGGCTGAAGACCCCAGTGGCGATTCAGCCCCAGCAGCACCCCTG
241 ---------+---------+---------+---------+---------+---------+
    P  S  T  K  I  K  A  E  D  P  S  G  D  S  A  P  A  A  P  L

    CCCCCTCAGCCGGCCCAGCCTCATCTGCCCCAGGCCCAACTCATGTTGACGGGCAGCCAG
301 ---------+---------+---------+---------+---------+---------+
    P  P  Q  P  A  Q  P  N  L  P  Q  A  Q  L  M  L  T  G  S  Q

    CTAGCTGGGGACATACAGCAGCTCCTCCAGCTCCAGCAGCTGGTGCTTGTGCCAGGCCAC
361 ---------+---------+---------+---------+---------+---------+
    L  A  G  D  I  Q  Q  L  L  Q  L  Q  Q  L  V  L  V  P  G  H

    CACCTCCAGCCACCTGCTCAGTTCCTGCTACCGCAGGCCCAGCAGAGCCAGCCAGGCCTG
421 ---------+---------+---------+---------+---------+---------+
    H  L  Q  P  P  A  Q  F  L  L  P  Q  A  Q  Q  S  Q  P  G  L

    CTACCGACACCAAATCTATTCCAGCTACCTCAGCAAACCCAGGGAGCTCTTCTGACCTCC
481 ---------+---------+---------+---------+---------+---------+
    L  P  T  P  H  L  F  Q  L  P  Q  Q  T  Q  G  A  L  L  T  S

    CAGCCCCGGGCCGGGCTTCCCACACAGGCCGTGACCCGCCCTACGCTGCCCGACCCGCAC
541 ---------+---------+---------+---------+---------+---------+
    Q  P  R  A  G  L  P  T  Q  A  V  T  R  P  T  L  P  D  P  H

    CTCTCGCACCCGCAGCCCCCCAAATGCTTGGAGCCACCATCCCACCCCGAGGAGCCCAGT
601 ---------+---------+---------+---------+---------+---------+
    L  S  H  P  Q  P  P  K  C  L  E  P  P  S  H  P  E  E  P  S

    GATCTGGAGGAGCTGGAGCAATTGGCCCGCACCTTCAAGCAACGCCGCATCAAGCTGGGC
661 ---------+---------+---------+---------+---------+---------+
    D  L  E  E  L  E  Q  F  A  R  T  F  K  Q  R  R  I  K  L  G

    TTCACGCAGGGTGATGTGGGCCTGGCCATGGGCAAGCTCTACGCCAACGACTTCAGCCAG
721 ---------+---------+---------+---------+---------+---------+
    F  T  Q  G  D  V  G  L  A  M  G  K  L  Y  G  N  D  F  S  Q
                   C  G  P  G  H  G  Q  A  L  R  Q  R  L  Q  P  D
```

FIG. 18A

```
      GTTACTACCTTATCCTCAGCTGTGGGGACGCTCCACCCCAGCCGGACAGCTGGAGGGGGT
1261  ---------+---------+---------+---------+---------+---------+
      V  T  T  [L]S  S  A  V  G  T  [L]H  P  S  R  T  A  G  G  G
        Y  Y  L  I  L  S  C  G  D  A  P  P  Q  P  D  S  N  M  G  W

      GGGGGCGGGGGCGGGGCTGCGCCCCCCCTCAATTCCATCCCCTCTGTCACTCCCCCACCC
1321  ---------+---------+---------+---------+---------+---------+
      G  G  G  G  G  A  A  P  P  L  N  S  I  P  S  V  T  P  P  P
        G  M  G  R  G  C  A  P  P  Q  F  H  P  L  C  H  S  P  T  P

      CCGGCCACCACCAACAGCACAAACCCCAGCCCTCAAGGCAGCCACTCGGCTATCGGCTTG
1381  ---------+---------+---------+---------+---------+---------+
      P  A  T  T  N  S  T  N  P  S  P  Q  G  S  H  S  A  I  G  L
        G  H  N  Q  Q  H  K  P  Q  P  S  R  Q  P  L  G  Y  M  L  V

      TCAGGCCTGAACCCCAGCACGGGGTAAGTGGGTGCACGTGGGAAGCTGTGGGGAGAAGCA
1441  ---------+---------+---------+---------+---------+---------+
      S  G  L  H  P  S  T  G  +
        A  P  E  P  Q  N  G  V  S  G  C  T  W  E  A  V  G  R  S  R

      GCGTCGCTGCTCCTTCTAGGGTGGGGAGCGGCACCCCAGTTATGTTGGCAGGTCCCTGCC
1501  ---------+---------+---------+---------+---------+---------+
        V  A  A  A  S  R  V  G  S  G  T  P  V  M  L  A  G  P  C  P

      CCTGCTAATGCCTCTGCTTTGCCTCTTGCAGAAGCACAATGGTGGGGTTGAGCTCCGGCT
1561  ---------+---------+---------+---------+---------+---------+
        C  +

      GAGTCCAGCCCTCATGAGCAACAACCCTTTGGCCACTATCCAAGGTGCGTGCTGCCTCAT
1621  ---------+---------+---------+---------+---------+---------+

      GTCACACCCATCGTCACCAGCCCCGGAATTCGAG
1681  ---------+---------+---------+----
```

FIG.18A (CONT.)

```
      ACGACCATTTCCCGCTTCGAGGCCCTCAACCTGAGCTTCAAGAACATGTGCAAACTCAAG
781   ---------+---------+---------+---------+---------+---------+
      T  T  I  S  R  F  E  A  L  N  L  S  F  K  N  M  C  K  L  K
        D  H  F  P  L  R  G  P  Q  P  E  L  Q  E  H  V  Q  T  Q  A

      CCCCTCCTGGAGAAGTGGCTCAACGATGCAGAGACTATGTCTGTGGACTCAAGCCTGCCC
841   ---------+---------+---------+---------+---------+---------+
      P  L  L  E  K  W  L  N  D  A  E  T  M  S  V  D  S  S  L  P
        P  P  G  E  V  A  Q  R  C  R  D  Y  V  C  G  L  K  P  A  Q

      AGCCCCAACCAGCTGAGCAGCCCCAGCCTGGGTTTCGAGCCTGCCGGCCGGAGACGCAAG
901   ---------+---------+---------+---------+---------+---------+
      S  P  N  O  L  S  S  P  S  L  G  F  E  P  A  G  R  R  R  K
        P  Q  P  A  E  Q  P  Q  P  G  F  R  A  C  M  P  E  T  Q  E

      AAGAGGACCAGCATCGAGACAAACGTCCGCTTCGCCTTAGAGAAGAGTTTTCTAGCGAAC
961   ---------+---------+---------+---------+---------+---------+
      K  R  T  S  I  E  T  N  V  R  F  A  L  E  K  S  F  L  A  N
        E  D  Q  M  R  D  K  R  P  L  R  L  R  E  E  F  S  S  E  P

      CAGAAGCCTACCTCAGAGGAGATCCTGCTGATCGCCGAGCAGCTGCACATGGAGAAGGAA
1021  ---------+---------+---------+---------+---------+---------+
                           <-------------------->        <--------
      Q  K  P  T  S  E  E  I  L  L  I  A  E  Q  L  H  M  E  K  E
        E  A  Y  L  R  G  D  P  A  D  R  R  A  A  A  H  G  E  G  S

      GTGATCCGCGTCTGGTTCTGCAACCGGCCCCAGAAGGACAAACGCATCAACCCCTGCAGT
1081  ---------+---------+---------+---------+---------+---------+
      ------------------>
      V  I  R  V  W  F  C  N  R  R  Q  K  E  K  R  I  H  P  C  S
        D  P  R  L  V  L  Q  P  A  P  E  G  E  T  H  Q  P  L  Q  C

      GCGGCCCCCATGCTGCCCAGCCCAGGGAAGCCGGCCAGCTACAGCCCCCATATGGTCACA
1141  ---------+---------+---------+---------+---------+---------+
      A  A  P  M  L  P  S  P  G  K  P  A  S  Y  S  P  H  H  V  T .
        G  P  H  A  A  Q  P  R  E  A  G  Q  L  Q  P  P  Y  G  H  T

      CCCCAAGGCGGCGCGGGGACCTTACCGTTGTCCCAAGCTTCCAGCAGTCTGAGCACAACA
1201  ---------+---------+---------+---------+---------+---------+
      P  Q  G  G  A  G  T  L  P [L] S  Q  A  S  S  S [L] S  T  T .
        P  A  G  R  G  D  L  T  V  V  P  S  F  Q  Q  S  E  H  N  S
```

FIG.18A (CONT.)

```
                                                                                 ↓
     CCTCAAGGCAGCCACTCGGCTATCGGCTTGTCAGGCCTGAACCCCAGCACGGGCCCTGGC
1411 ---------+---------+---------+---------+---------+---------+
     P  Q  G  S  H  S  A  I  G  L  S  G  L  N  P  S  T  G  P  G
       S  A  Q  P  L  G  Y  R  L  V  M  P  E  P  Q  M  G  P  N  P

     CTCTGGTGGAACCCTGCCCCTTACCAGCCTTGATGGCAGCGGGAATCTGGTGCTGGGGGC
1471 ---------+---------+---------+---------+---------+---------+
     L  W  W  N  P  A  P  Y  Q  P  .
       L  V  E  P  C  P  L  P  A  L  M  A  A  G  I  W  C  W  G  Q

     AGCCGGTGCAGCCCCGGGGAGCCCTGGCCTGGTGACCTCGCCGCTCTTCTTGAATCATGC
1531 ---------+---------+---------+---------+---------+---------+
       P  V  Q  P  R  G  A  L  A  W  .

     TGGGCTGCCCCTGCTCAGCACCCCGCCTGGTGTGGGCCTGGTCTCAGCAGCGGCTGCGGG
1591 ---------+---------+---------+---------+---------+---------+

     TGTGGCAGCCTCCATCTCCAGCAAGTCTCCTGGCCTCTCCTCCTCATCCTCTTCATCCTC
1651 ---------+---------+---------+---------+---------+---------+

     ATCCTCCTCCTCCTCCACTTGCAGCGAGACGGCAGCACAGACCCTGGAGGTCCAGGGGGG
1711 ---------+---------+---------+---------+---------+---------+

     CCCGAGGCAGGGTCCAAACCTGAGTGAGGGCCAGCCATGCCTCCCCTCCCATTCCTCTGG
1771 ---------+---------+---------+---------+---------+---------+

     TCCCTGCCCCGGAATTC
1831 ---------+-------
```

FIG.18B

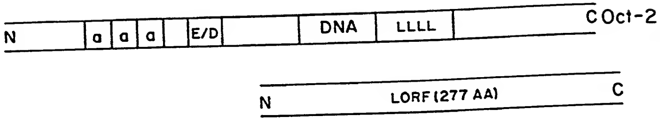


FIG.18C

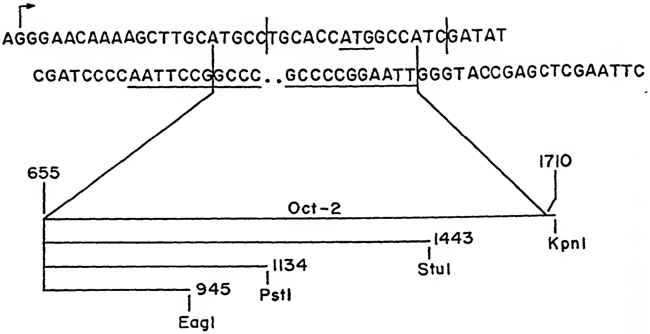

AGGGAACAAAAGCTTGCATGCCTGCACCATGGCCATCGATAT
CGATCCCCAATTCCGGCCC..GCCCCGGAATTGGGTACCGAGCTCGAATTC
655
1710
Oct-2
1443
KpnI
1134
StuI
945
PstI
EagI

FIG.19

```
                                         helix  turn helix
                                         <------>  <-------->
Oct-2      RRKKRTSIETNVRFALEKSFLANQKPTSEEILLIAEQLHMEKEVIRVWFCNRRQKEKRINPC
                                             *         *
a1         SPKGKSSISPQARAFLEQVFRRKQSLNSKEKEEVAKKCGITPLQVRVWFINKRMRSK
                                             *   *     *
α2         KPYRGHRFTKENVRILESWFAKNPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKTIT
                                                       *
pho2       QRPKRTRAKGEALDVLKRKFEINPTPSLVERKKISDLIGMPEKNVRIWFQNRRAKLRKKQ
                                                 *     *
mec-3      RRGPRTTIKQNQLDVLNEMFSNTPKPSKHARAKLALETGLSMRVIQVWFQNRRSKERRLK
                                             *   *     *

cut        SKKQRVLFSEEQKEALRLAFALDPYPNVGTIEFLANELGLATRTITNWFHNHRMRLKQQV
                                             *   *     *
en         EKRPRTAFSSEQLARLKREFNENRYLTERRRQQLSSELGLNEAQIKIWFQNKRAKIKKST
                                                 *     *
Antp       RKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKEN
                                             *         *
                                                                   (conserved
               R      Q   L        Y              L       WF N R   residues in
                                                                   homeo-box
                                                                   family)
```

FIG.20

FIGURE 21A

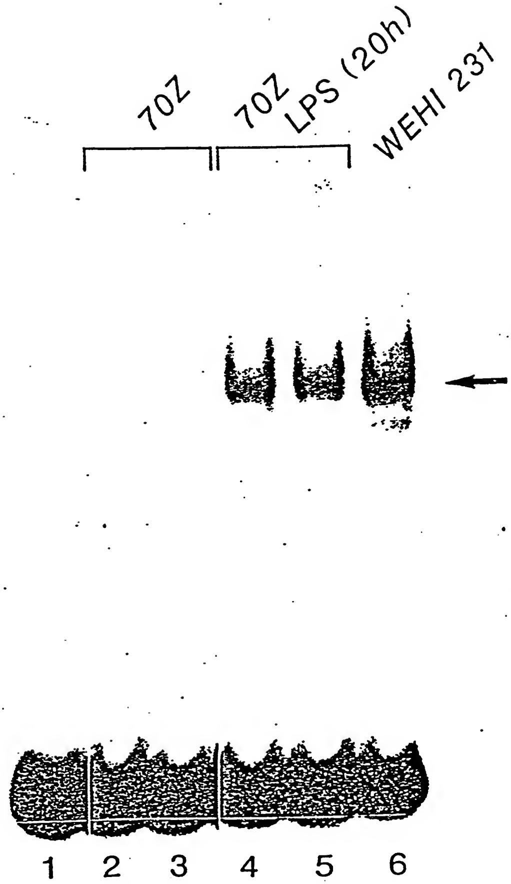
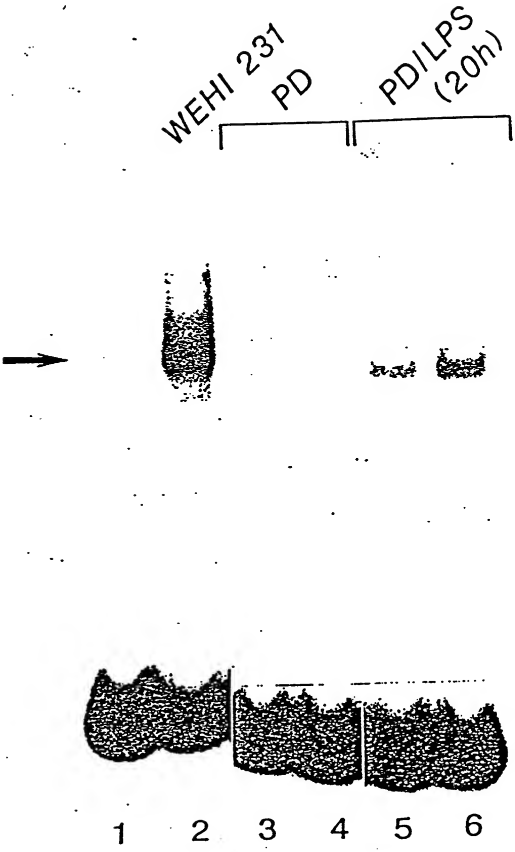


FIGURE 21B



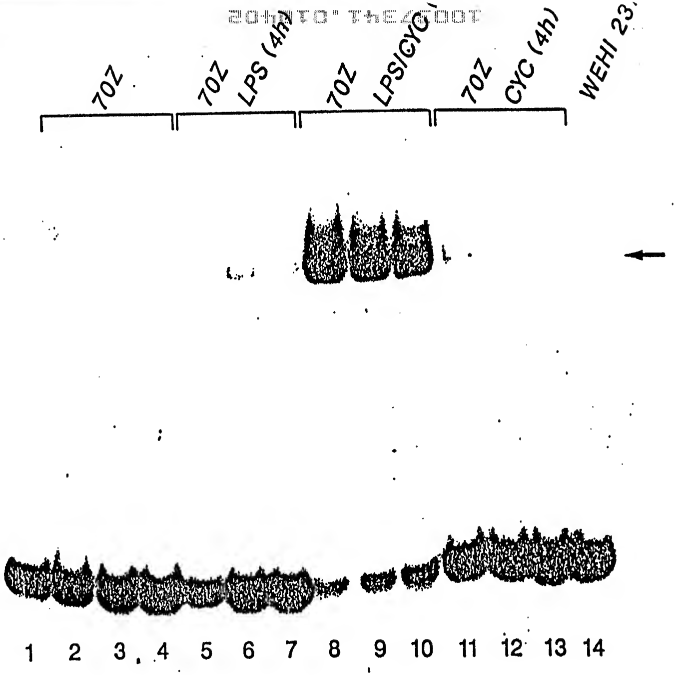

70Z
70Z
LPS (4h)
70Z
LPS/CYC
70Z
CYC (4h)
WEHI 23.
1
2
3
4
5
6
7
8
9
10
11
12
13
14

FIGURE 22A

FIGURE 22B

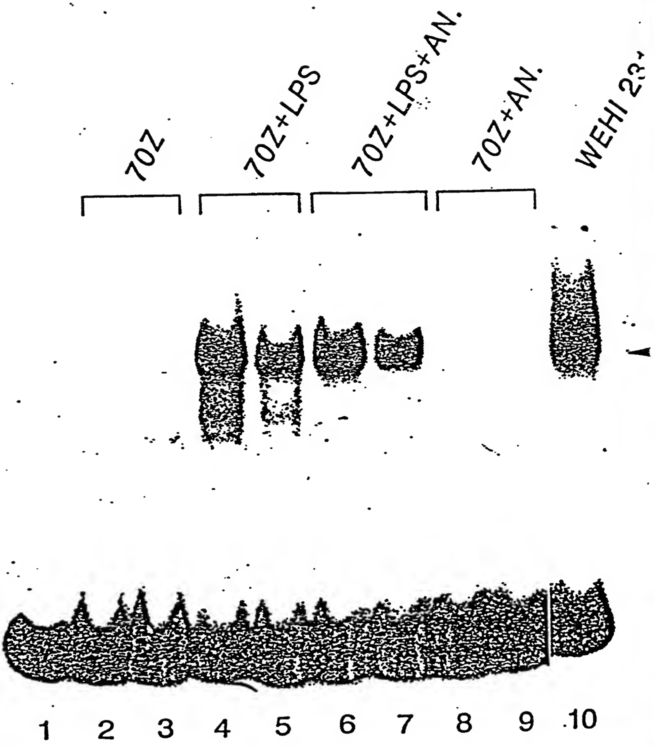


FIGURE 23A

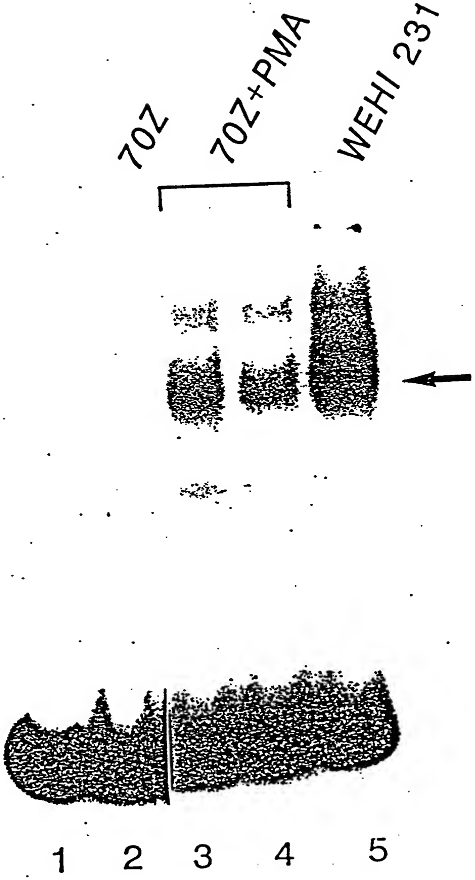


FIGURE 23B

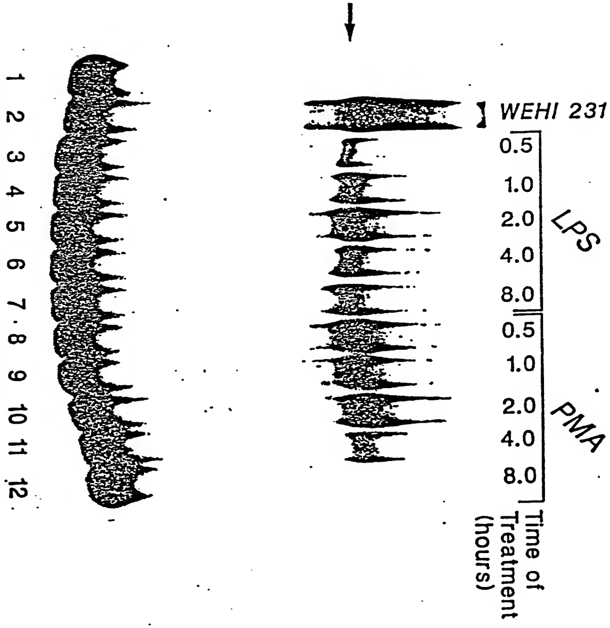

WEHI 231
0.5
1.0
2.0
4.0
8.0
LPS
0.5
1.0
2.0
4.0
8.0
PMA
Time of Treatment (hours)
1
2
3
4
5
6
7
8
9
10
11
12

FIGURE 24A

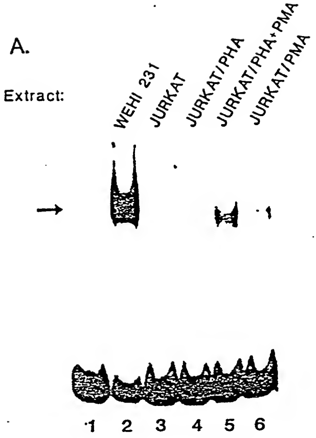


FIGURE 24B

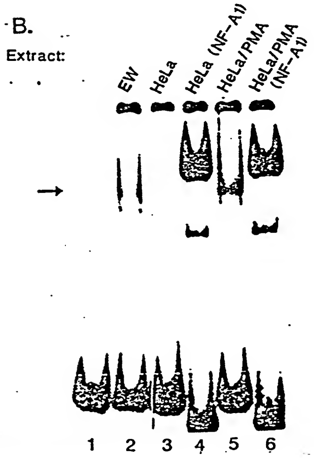


FIGURE 24C

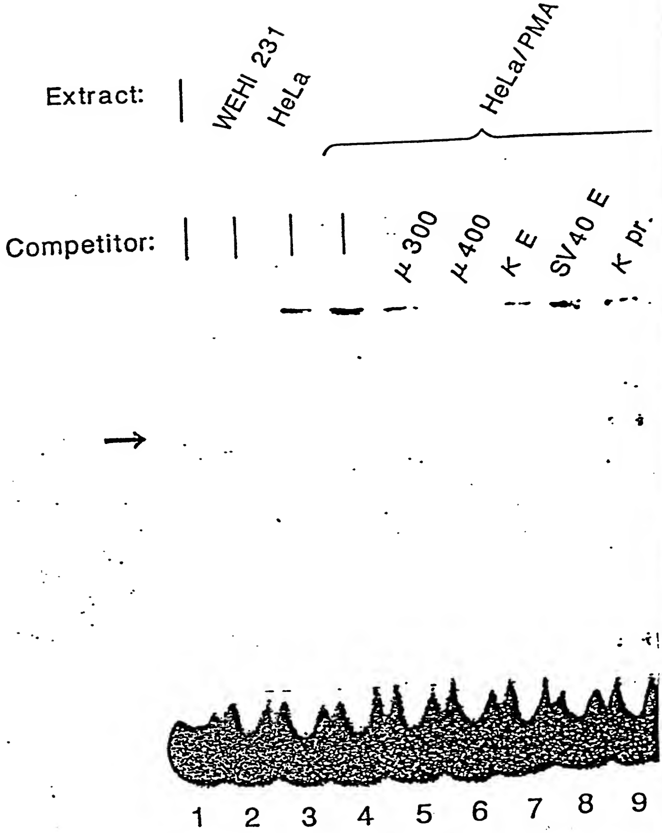
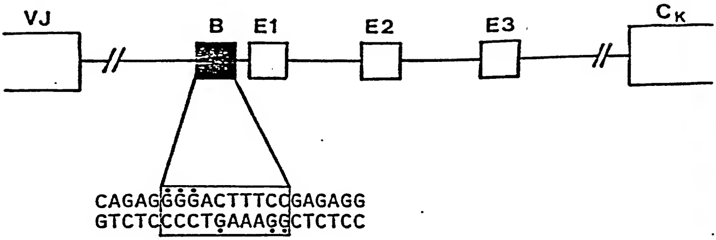

Extract:
WEHI 231
HeLa
HeLa/PMA
Competitor:
μ 300
μ 400
κ E
SV40 E
κ pr.
1
2
3
4
5
6
7
8
9

FIGURE 25

κ-Enhancer



HIV LTR

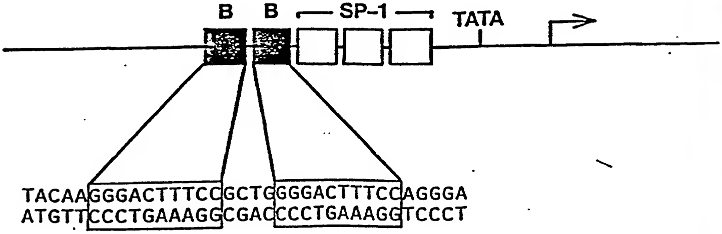


FIGURE 26

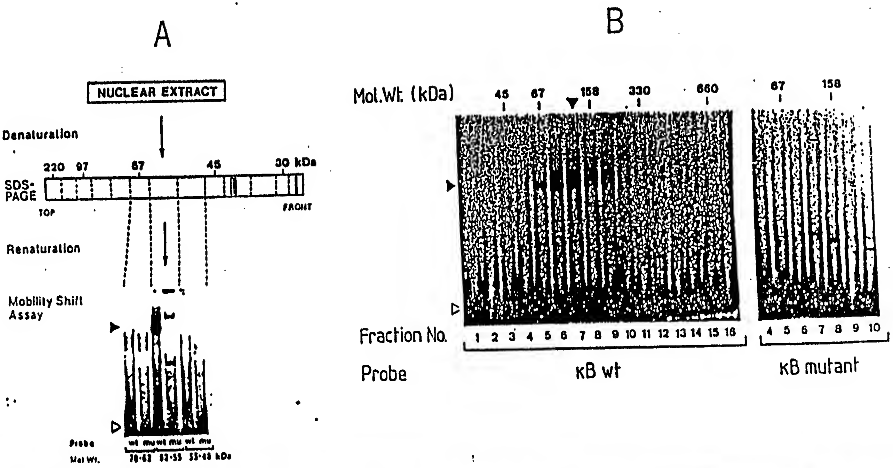

A
NUCLEAR EXTRACT
Denaturation
SDS-PAGE
220
97
67
45
30 kDa
TOP
FRONT
Renaturation
Mobility Shift Assay
Probe
wt
mu
wt
mu
wt
mu
Mol Wt.
70-62
62-55
55-48 kDa
B
Mol.Wt. (kDa)
45
67
158
330
660
67
158
Fraction No.
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
4 5 6 7 8 9 10
Probe
κB wt
κB mutant

FIGURE 27

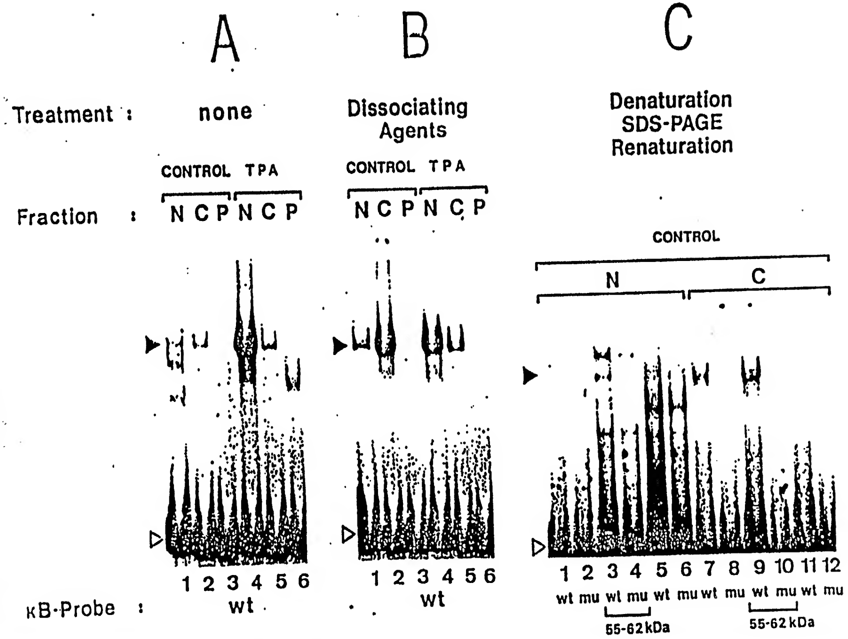

A
B
C
Treatment :
none
Dissociating Agents
Denaturation SDS-PAGE Renaturation
CONTROL
TPA
CONTROL
TPA
Fraction :
N C P N C P
N C P N C P
CONTROL
N
C
1 2 3 4 5 6
1 2 3 4 5 6
1 2 3 4 5 6 7 8 9 10 11 12
κB-Probe :
wt
wt
wt mu wt mu wt mu wt mu wt mu wt mu
55-62 kDa
55-62 kDa

FIGURE 28

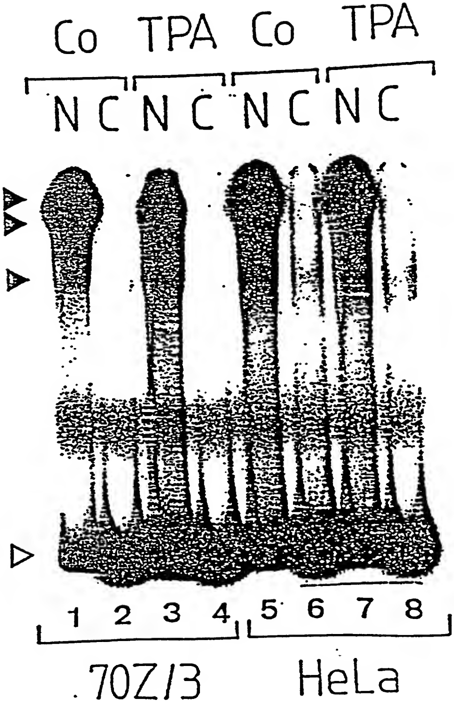


FIGURE 29

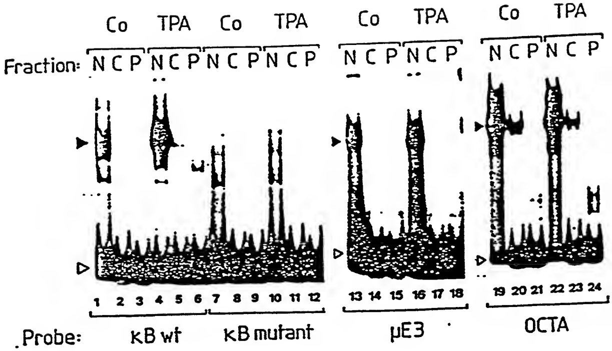


FIGURE 30

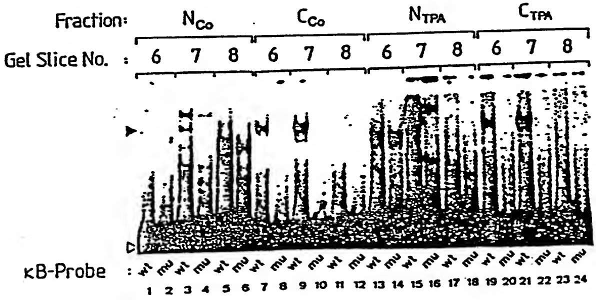


FIGURE 31

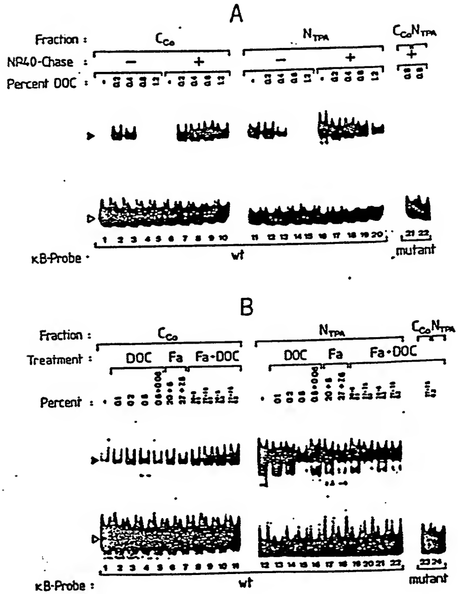

A
Fraction :
C_{Co}
N_{TPA}
$C_{Co}N_{TPA}$
NP40-Chase :
−
+
−
+
+
Percent DOC :
1 2 3 4 5 6 7 8 9 10
11 12 13 14 15 16 17 18 19 20
21 22
κB-Probe :
wt
mutant
B
Fraction :
C_{Co}
N_{TPA}
$C_{Co}N_{TPA}$
Treatment :
DOC
Fa
Fa·DOC
DOC
Fa
Fa·DOC
Percent :
1 2 3 4 5 6 7 8 9 10 11
12 13 14 15 16 17 18 19 20 21 22
23 24
κB-Probe :
wt
mutant

FIGURE 32

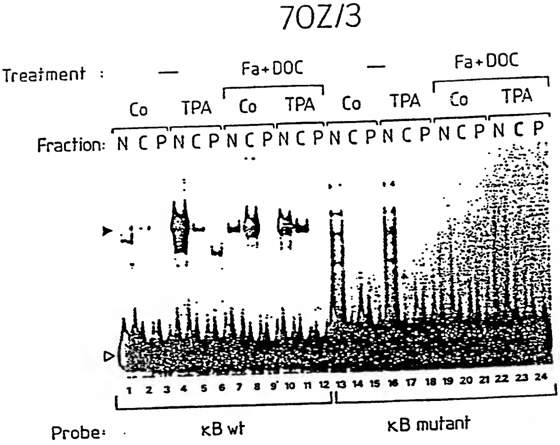


FIGURE 33

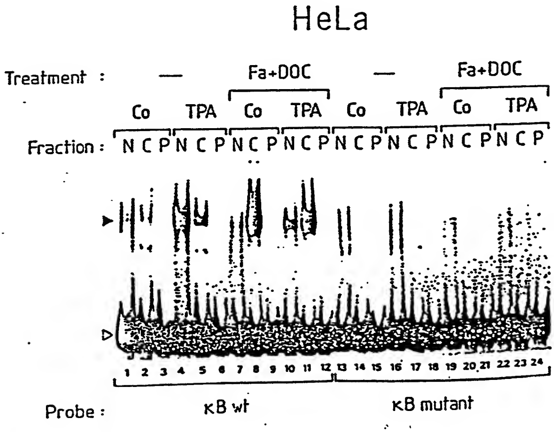


FIGURE 34

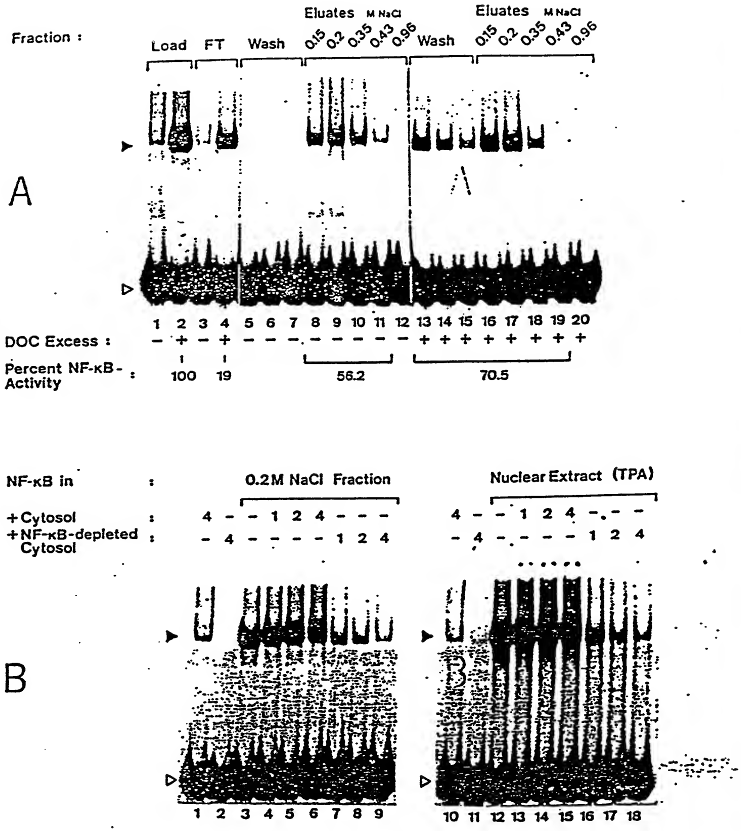

A
Fraction :
Load
FT
Wash
Eluates M NaCl
0.15 0.2 0.35 0.43 0.96
Wash
Eluates M NaCl
0.15 0.2 0.35 0.43 0.96
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
DOC Excess : − + − + − − − − − − − − + + + + + + + +
Percent NF-κB-Activity : 100 19 56.2 70.5
B
NF-κB in :
0.2M NaCl Fraction
Nuclear Extract (TPA)
+Cytosol : 4 − − 1 2 4 − − − 4 − − 1 2 4 − − −
+NF-κB-depleted Cytosol : − 4 − − − − 1 2 4 − 4 − − − − 1 2 4
1 2 3 4 5 6 7 8 9
10 11 12 13 14 15 16 17 18

FIGURE 35

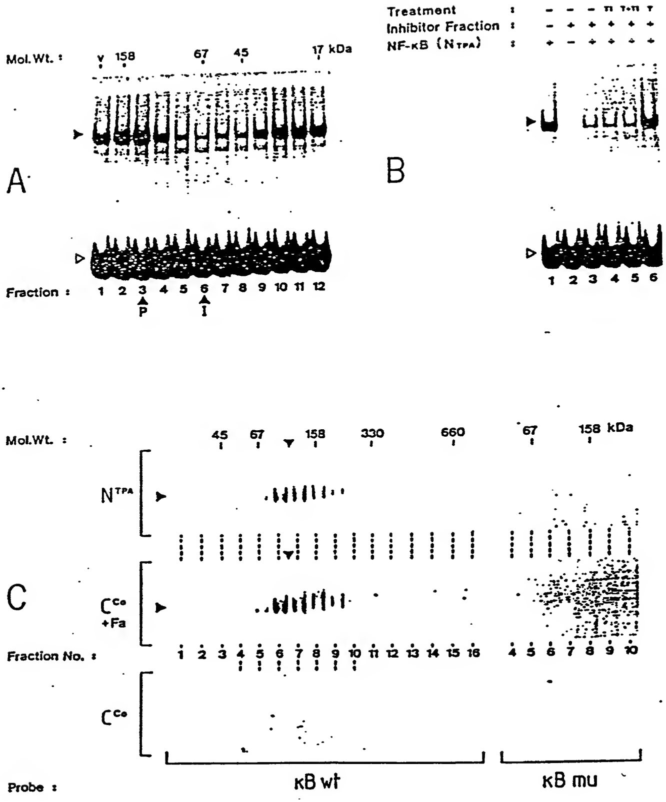

Mol.Wt. :
158
67
45
17 kDa
A
Fraction :
1 2 3 4 5 6 7 8 9 10 11 12
P
I
Treatment :
Inhibitor Fraction :
NF-κB (NTPA) :
B
1 2 3 4 5 6
Mol.Wt. :
45
67
158
330
660
67
158 kDa
C
NTPA
CCo +Fa
Fraction No. :
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
4 5 6 7 8 9 10
CCo
Probe :
κB wt
κB mu

FIGURE 36

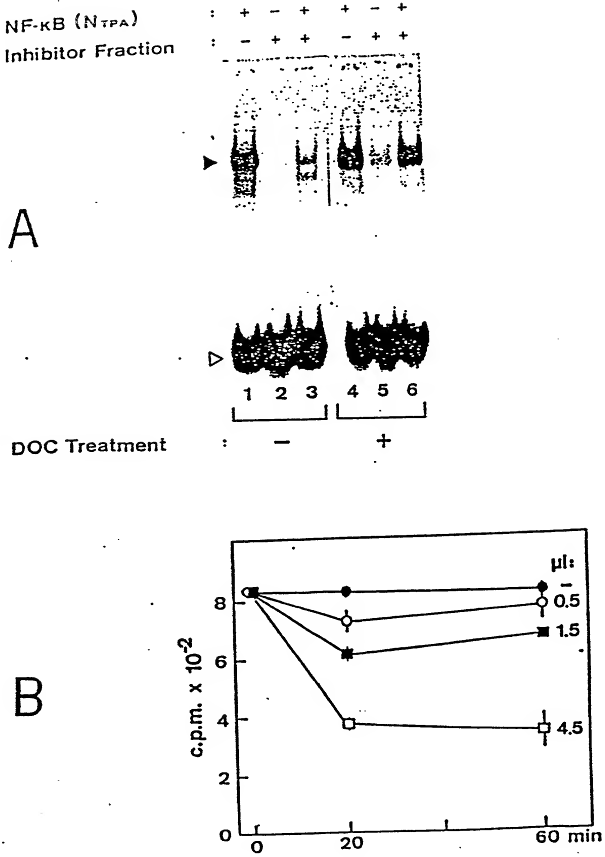

NF-κB (N_TPA) : + − + + − +
Inhibitor Fraction : − + + − + +
A
1 2 3 4 5 6
DOC Treatment : − +
B
c.p.m. x 10^-2
0
2
4
6
8
0
20
60 min
µl:
−
0.5
1.5
4.5

FIGURE 37

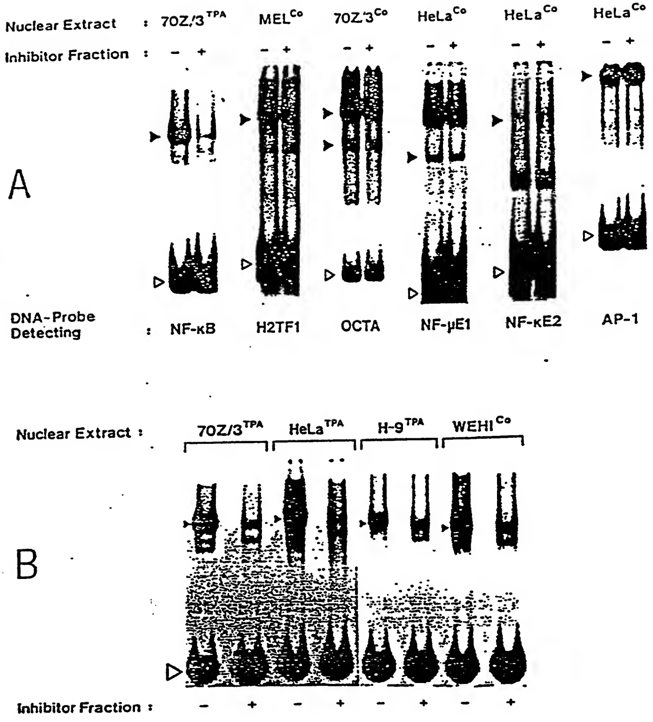
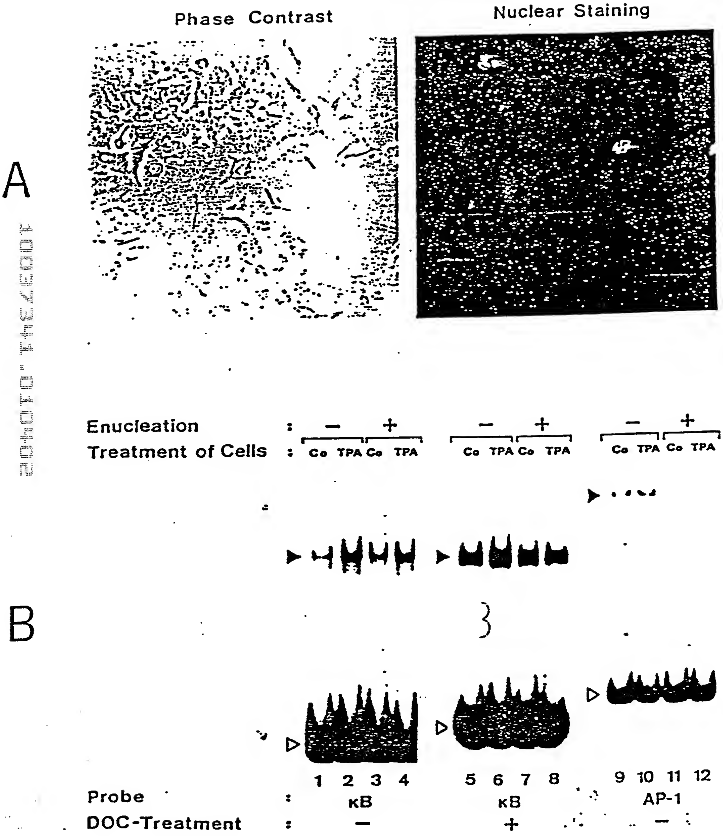

Nuclear Extract : 70Z/3 TPA MEL Co 70Z/3 Co HeLa Co HeLa Co HeLa Co
Inhibitor Fraction : – + – + – + – + – + – +
A
DNA-Probe Detecting : NF-κB H2TF1 OCTA NF-μE1 NF-κE2 AP-1
Nuclear Extract : 70Z/3 TPA HeLa TPA H-9 TPA WEHI Co
B
Inhibitor Fraction : – + – + – + – +

FIGURE 38


A
Phase Contrast
Nuclear Staining
B
Enucleation : − + − + − +
Treatment of Cells : Co TPA Co TPA Co TPA Co TPA Co TPA Co TPA
1 2 3 4 5 6 7 8 9 10 11 12
Probe : κB κB AP-1
DOC-Treatment : − + −

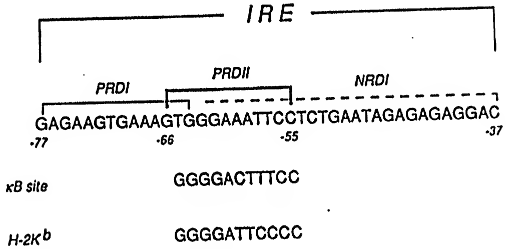

IRE
PRDI
PRDII
NRDI
GAGAAGTGAAAGTGGGAAATTCCTCTGAATAGAGAGAGGAC
-77
-66
-55
-37
κB site
GGGGACTTTCC
H-2K^b
GGGGATTCCCC

Figure 39

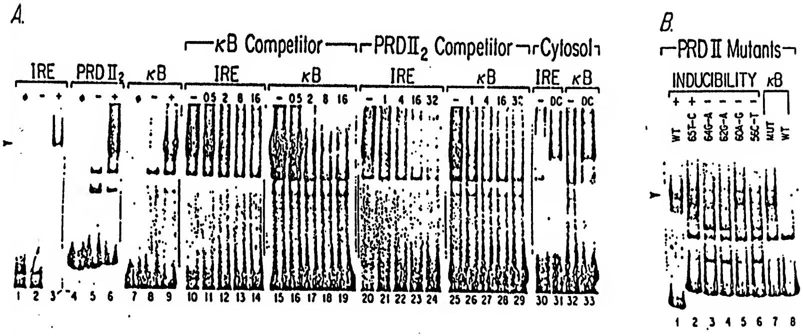

A.
κB Competitor
PRDII2 Competitor
Cytosol
IRE
PRD II2
κB
IRE
κB
IRE
κB
IRE
κB
• - +
• - +
• - +
- 05 2 8 16
- 05 2 8 16
- 1 4 16 32
- 1 4 16 32
- DC
- DC
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33
B.
PRD II Mutants
INDUCIBILITY
κB
+ + - - - -
WT
65T-C
64G-A
62G-A
60A-G
56C-T
MUT
WT
1 2 3 4 5 6 7 8

Figure 40

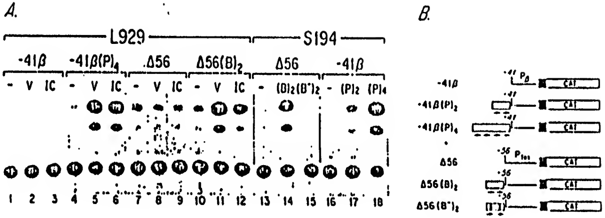

A.
L929
S194
-41β
-41β(P)4
Δ56
Δ56(B)2
Δ56
-41β
- V IC - V IC - V IC - V IC - (B)2(B')2 - (P)2 (P)4
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
B.
-41β
-41β(P)2
-41β(P)4
Δ56
Δ56(B)2
Δ56(B')2
-41
Pβ
-56
Pfos
CAT

Figure 41

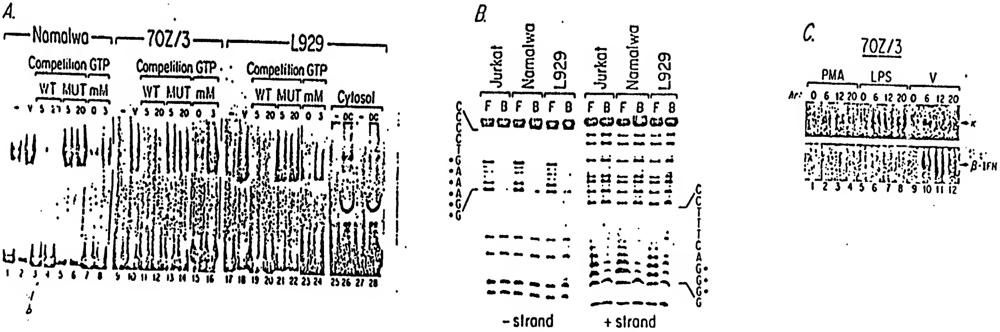

A.
Namalwa
70Z/3
L929
Competition GTP
WT MUT mM
- V 5 20 5 20 0 3
Cytosol
- DC - DC
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
B.
Jurkat
Namalwa
L929
F B F B F B
C C C C T G A A A G G
C C T T T C A G G G G
- strand
+ strand
C.
70Z/3
PMA
LPS
V
hr: 0 6 12 20 0 6 12 20 0 6 12 20
κ
β-IFN
1 2 3 4 5 6 7 8 9 10 11 12

Figure 42

```
115   [illegible]
239   [illegible]
359   [illegible]
479   [illegible]
599   [illegible]
719   [illegible]
839   [illegible]
959   [illegible]
1079  [illegible]
                                                   M T P P P P K V R    9
1199  [illegible]

1319  [illegible]
      F L P R I K G G E G G G P W P I S L H C V T K V L L L P V N I L N Y F S P D I L    49

1439  [illegible]
      K R A V V R P L E G I F A L G Y P P P A Y A A A P N R P A S S A A M L S A H S P    89

1559  [illegible]
      A E P P A V K Q C K P P K K R R Q G G L L P P D D R N D S G L D S H K M E E Y R    129

1679  [illegible]
      Q L V R K L K D I K L Q P R E P P A R P N A H A Q Q L T H D G Q T P L H L A I I    169

1799  [illegible]
      N E R K K A L S L E Y I N Q A A G D A A F L N F Q N N L S Q T P L H L A V I T D Q    209
       Ank. I                                                                  Ank. II
1919  [illegible]
      A R T A K N L L N A D G C D L D V K D F N G K T P L H I A C Q Q G S L R S Y A Y L    249
                                                                      Ank. III
2039  [illegible]
      T Q H C Q P N K L L A V L Q A T N Y N G H T C L H L A S I Q G Y L A Y V R Y L L    289
                                                                      Ank. IV
2159  [illegible]
      S L G A D V N A Q E P C K G R T A L H L A V D L Q N S D L V S L L V K H G A D V    329
                                                         Ank. V
2279  [illegible]
      N K V T Y Q G Y S P Y Q L T W A R T T P A Y R S E    354

2399  [illegible]
2519  [illegible]
2639  [illegible]
2759  [illegible]
2879  [illegible]
2999  [illegible]    3106
3119  [illegible]
```

FIGURE 43